

SEQUENCE LISTING

<110> Donoho, Gregory
Turner, C. Alexander Jr.
Nehls, Michael
Friedrich, Glenn
Zambrowicz, Brian
Sands, Arthur T.

<120> Novel Human Proteins and Polynucleotides
Encoding the Same

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<150> US 60/160,285

<151> 1999-10-19

<150> US 60/183,583

<151> 2000-02-18

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<212> DNA

<213> homo sapiens

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Val Pro Lys Glu Leu Leu Asn Thr Ser Glu Val Thr Val Arg Phe
65 70 75 80
Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala
85 90 95
Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu Arg Ala Ser His
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Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp
115 120 125
Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly Tyr Arg Asp Thr
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Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly Ile Ser Arg Tyr
165 170 175
Glu Gly Ile Leu Ala Asn Gly Val Leu Ser Arg Asp Gly Ser Leu Ser
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Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser Arg Ser Leu Ser
195 200 205
Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser Trp Gln Ser Val
210 215 220
Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly Gln Ala Arg Leu
225 230 235 240
Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser Ser Asn Asn His
245 250 255
Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu Lys Lys Lys Ile
260 265 270
Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn Phe Asn Phe Tyr
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Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn Ser Lys Trp Lys
290 295 300
Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val Phe Gln Gly Asn
305 310 315 320
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Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His Gln Arg Ile Ala
340 345 350
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370 375 380
Glu Asp Glu Thr Ile Thr Arg Pro Ile Pro Ser Glu Glu Thr Ser Thr
385 390 395 400

Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val Leu Leu Val Val
 405 410 415
 Leu Val Phe Ala Gly Met Gly Ile Phe Ala Ala Phe Arg Lys Lys Lys
 420 425 430
 Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln Lys Thr Asp Cys
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 Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln Ser Ala Glu Phe
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<213> homo sapiens

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 50 55 60
 Gly Leu Leu Ala Leu Leu Ala Val Ser Ala Pro Leu Arg Leu Gln
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 Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu Val Thr Tyr Gln Asp
 85 90 95
 Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly Thr Tyr Pro Asn His
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 Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu Ile
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 Tyr Leu Leu Phe Thr Ser Ser Asp Gln Tyr Gly Pro Tyr Cys Gly
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 Ser Met Thr Val Pro Lys Glu Leu Leu Asn Thr Ser Glu Val Thr
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 Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu Leu
 180 185 190
 Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu Arg
 195 200 205
 Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala Gly
 210 215 220
 Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly Tyr
 225 230 235 240
 Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile
 245 250 255
 Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly Ile
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 275 280 285
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 Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser Ser
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 Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu Lys
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 Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn Phe
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 Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His Gln
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 Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val Ser
 465 470 475 480
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 485 490 495
 Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val Leu
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 515 520 525
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 530 535 540
 Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln Ser
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attctgaggt	tggagattt	ggatatcgaa	tccagacct	gtgcttctga	ctatcttc	300
ttcaccagct	cttcagatca	atatggtcca	tactgtggaa	gtatgactgt	tcccaaagaa	360
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Asp Tyr Leu Leu Phe Thr Ser Ser Asp Gln Tyr Gly Pro Tyr Cys
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Gly Ser Met Thr Val Pro Lys Glu Leu Leu Asn Thr Ser Glu Val
115 120 125
Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu
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145 150 155 160
Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala
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Gly Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly
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225 230 235 240
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Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser
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275 280 285
Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser
290 295 300
Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu
305 310 315 320
Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn
325 330 335
Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn
340 345 350
Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val
355 360 365
Phe Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln Asn Asn Phe Ile
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Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His
385 390 395 400
Gln Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys Gln Ile Thr Gln
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Gly Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val

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Glu Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val		
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Arg Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln		
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Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln		
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<211> 1768

<212> DNA

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